3

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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 1, 2005, 14:20:08; Search time 40 Seconds (without alignments) 582.111 Million cell updates/sec Run on:

US-10-629-329A-2 1322 1 MSGCDAGEGDCCSRRCGAQD.....SMKKVGLDPSQLPVGENGIV 242 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote		Ω	conserved hypothet	L-fuculose-phospha	probable sugar ald	L-fuculose-phospha	L-fuculose-phospha	L-fuculose-phospha	L-ribulose-phospha	conserved hypothet	hypothetical prote	probable sugar iso	1-fuculose phospha	L-ribulose-phospha	sugar isomerase sg		L-ribulose-5-phosp	L-ribulose-phospha	L-ribulose-phospha	L-ribulose-phospha	L-ribulose-phospha	probable epimerase	probable epimerase	sugar isomerase Sg	L-ribulose-phospha	fuculose-1-phospha	L-fuculose-phospha	L-fuculose-phospha
SUMMARIES	ID		T27523	T39191	A69864	H70469	D83436	C69054	A64477	A72396	S47804	E82587	A95238	AI0977	AC3533	B98102	G90586	AD1052	G83883	E69587	H64108	S56423	AI0271	F91275	F86116	B82484	S73671	H84275	E71241	ADECEP
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	Query Match Length	244	284	192	209	208	202	191	181	254	231	218	227	231	244	234	243	228	231	229	243	228	231	228	228	230	242	211	189	215
de	Query	37.4	32.6	20.8	16.3	14.6	12.6	11.8	11.5	11.4	11.0	10.9	10.7	10.7	10.6	10.4	10.0	9.9	9.9	9.8	9.8	9.8	9.7	9.7	9.7	9.6	9.5	9.3	9.5	9.1
	Score	495	431.5	274.5	215.5	192.5	166	156.5	152	151	145	144	142	141	140.5	137	132	131	131	130	129.5	129	128.5	128	128	127	126	123	122	120.5
	Result No.	-	7	n	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18		20	21	22	23	24	25	26		28	29

L-ribulose-phospha L-fuculose-1-phosp L-fuculose-1-phosp	L-fuculose-phospha probable aldolase, fuculose-1-phospha	L-ribulose-phospha L-fuculose phospha L-fuculose-phospha	ribulose-5-phospha 1-fuculose phospha L-ribulose-phospha	L-ribulose-5-phosp L-ribulose-5-phosp L-fuculose-phospha L-ribulose-5-phosp
AB0404 F85931 D91086	C64081 E96013 AH0862	ISEB4T C95253 A98118	B97065 AF3646 ISECP4	A85488 A90637 E72546 AB0515
000	466	- 70 70	0 0 H	2222
231 215 215	216 225 215	248 212 217	233 224 231	231 231 215 231
1.00	000	8.8 6.7 6.7	8 8 8 2 4 4	8 8 8 8 4 4 6 6
120.5	119	116.5 114.5 114.5	112.5	111.5 111.5 109.5 109.5
30	3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	36 37 38	39 41	4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

## ALIGNMENTS

RESULT 1 S57042 hypothetical protein YJR02- NyAlternate names: hypothetics C;Species: Saccharomyces c; C;Date: OB-Jul-1995 #seques C;Accession: S57042; S5703; R;Zagulski, M.; Babinska, submitted to the Protein S; A;Reference number: S57040 A;Accession: S57042 A;Molecule type: DNA	RESULT 1 S57042 hypothetical protein YJR024c - yeast (Saccharomyces cerevisiae) hypothetical protein J1545; hypothetical protein J1545; hypothetical protein YJR83.18 C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Date: 08-Jul-1995 #sequence revision 08-Sep-1995 #text_change 09-Jul-2004 C;Accession: S57042; S57043; S55213; 86503; 861120 R;Zaguleki, M; Babinska, B.; Gromadka, R.; Migdalski, A.; Rytka, J.; Sulicka, J.; Herbc. submitted to the Protein Sequence Database, September 1995 A;Reference number: S57040 A;Accession: S57042 A;Accession: S57042
A, Residues: 1-244 cHUA-NCOSS-references: UNIPRO' R, CAGES-references: UNIPRO' R, CHE HARAI, M.; Grivell, L., Submitted to the Protein SI A, Reference number: SS6771 A, Rocession: SS7039 A, Molecule type: DNA A, Residues: 44-244 < ZAG>A, CROSS-references: EMBL: ZAG>HCOSS-references: EMBL: ZAG>HOBMITTED to the EMBL DATA A, Reference number: SS5183 A, Accession: SS513	A.Residues: 1-244 <-HUA>. A.Residues: 1-244 <-HUA>. A.R.Crose-references: UNIPROT:P47095; EMBL:Z49524; NID:g1015662; PIDN:CAA89549.1; PID:g101 R.de Haan, M.; Grivell, L.A.; Smits, P.H.M. Submitted to the Protein Sequence Database, September 1995 A.Reference number: S56771 A.Accession: S57039 A.Residues type: DNA A.Residues: 44-244 <-ZAG> A.Residues: 44-244 <-ZAG> A.Residues: 44-244 <-ZAG> A.Residues: 42-24
A; Molecule type: DNA A; Residues: 44-24 < DEH> A; Cross-references: EMBL. R; Zagulski, M.; Babinska, Yeast 11, 1179-1186, 1999 A; Title: The sequence of A; Reference number: S605( A; Accession: S60503 A; Status: nucleic acid s6 A; Molecule type: DNA A; Residues: 1-244 < ZAF>	A; Molecule type: DNA A; Cross at 44-244 < DEB:> A; Cross at 42-244 < DEB:> A; Cross at 24-244 < DEB:> A; Cross at 24-244 < DEB: A; Migdalski, A.; Rytka, J.; Sulicka, J.; Herbe R; Zagulski, M.; Babinska, B.; Gromadka, R.; Migdalski, A.; Rytka, J.; Sulicka, J.; Herbe R; Asact and 1179-1186, 1995 A; Reference number: S60503 A; Reference number: S60503 A; Accession: S60503 A; Accession: S60503 A; Accession: S60503 A; Molecule type: DNA A; Residues: 1-244 < ZAF>
A;Cross-references: EMBL C;Genetics: SGD:: A;Cross-references: SGD:: A;Map position: 10R Query Match Best Local Similarity Matches 107; Conserv. Qy 18 AQDKEHPRYL:	EMBL:X87297; NID:g1129159; PIDN:CAA60719.1; PID:e183285 SGD:S0003785 37.4%; Score 495; DB 2; Length 244; ity 45.9%; Pred. No. 4e-37; servative 37; Mismatches 69; Indels 20; Gaps IPRYLIPELCKOPYHLGWVTGTGGGISLKHGDEIYIAPSGVQKERIOPEDMFV
Db 10 Si	10 SDDPCHPANLICTLCKQFFHNNWCTGTGGGISIKDPNTNYYYLAPSGVQKEKMIPEDLFV 69

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76 CDINEKD-ISGPSPSKKLKKSQCTPLFMNAYTMRGAGAVIHTHSKAAVMATLLFPGREFK 134

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C; Accesson: A69864
R; Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Berter, C; Accesson: A69864
R; Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Berter, C; Bron, S; Brouillet, S; Bruschi, C.V; Caldwell, B; Capuano, V; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C; Ferrari, E. Nature 390, 249-256, 1997
A; Athehors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, X.; Fuma, S.; Galizzi, A.; Galler, A; Athehors: Rouger, D.; Knoningstein, G; Krogh, S; Kumano, M.; Kurita, K; Lapidus, A.; Hullo, M.F. Koetter, P; Koningstein, G; Krogh, S; Kumano, M.; Kurita, K; Lapidus, A.; Hardinois, Koetter, P.; Koningstein, G; Rocha, B.; Rose, M.; Sadaie, Y; Scato, T; Scanhon, Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Scato, T; Scanhon, Rieger, M.; Tamakoshi, A.; Tanaka, T.; Terpeitra, P.; Tognoni, J.; Sekowska, A.; Scankera, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, V.; Voshida, K.; Vatu, K.; Yata, K.; Yoshida, K.; Witters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, V.; Yata, K.; Yoshida, K.; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus de Altiles. Altiles and Alti
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A;Cross-references: UNIPROT:031668; GB:299111; GB:AL009126; NID:g2633699; PIDN:CAB13234
A;Experimental source: strain 168
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                                                                                                                                                                      86 PSPSKKLKKSQCTPLFMNAYTWRGAGAVIHTHSKAAVWATLLFPGREFKITHQEMIKGIK 145
                                                                                                                                                                                                                                           204
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                                                                                         -----KDRVQRDFITENDIVTFNLSN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 SGPSPSKKLKKSQCTPLFMNAYTMRGAGAVIHTHSKAAVMATLLFPGREFKITH--QEMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 IPELCKOFYHLGWVTGTGGGISLKHGDE---IYIAPSGVQKERIQPEDMFVCDIN-EKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Species: Bacillus subtilis
C.Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                         146 KCT-SGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWGETW
                                           27 LIPELCKOFYHLGWVT-GTGGGISLKHGDEIYIAPSGVQKERIQPEDMFVCDINEKDISG
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  21;
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     76; Indels
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32.4%; Pred. No. 5.6e-12;
tive 32; Mismatches 87
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     29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LILELIPHFYSLGWMKFGSGYAICV---
                                                                                                                                                                                                                                                                                                                                               205 EKAKTMCECYDYLFDIAVSMK 225
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170 EKSKTQMECYEYLFELDYKLK 190
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            75; Conservative
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Best Local Similarity
Matches 66; Conserv
                 Matches
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision T2523
B;Reshaw, J.
S;Referance number: Z20382
A;Referance number: Z20382
A;Referance number: Z20382
A;Residues: PNA
A;Residues: 1-284 < WIL>
A;Residues: 1-284 < WIL>
A;Residues: 1-284 < WIL>
A;Experimental source: clone ZC373
A;Experimental source: clone ZC373
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                                                                       126 IANIEQIKAIPSGKVDPVTKKPMALSFF---DTLKIPHIENMAHEDELIDDLHKTFKDYP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 ELCKOFYHLGWVTGTGGGISLKHGDEIYIAPSGVQKERIQPEDMFVCDINEKDISGPSPS
                                                                                                                                                                      DSCAVLVRRHGVYVWGETWEKAKTMCECYDYLFDIAVSMKKVGLDPSQLPVGE
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Pred. No. 2.4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , 6e-31;
76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
32.6%; Score 431.5; DB 2;
Best Local Similarity 39.9%; Pred. No. 2.6e-31;
Matches 87; Conservative 34; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGYYRYDDMLVVPIJENTPEEKGL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Map position: X
A,Introns: 26/3; 75/2; 114/1; 236/2
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A;Introns: 27/2; 53/2; 73/2; 129/1
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A.Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; Alther Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A; Reference number: A64300; MUID:96337999; PMID:8688087
A.Accession: A4477
A.Science 173, 1058-10747
A.Science number: A64300
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A;Cross-references: UNIPROT:Q58813; GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB99428.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Methanobacterium thermoautotrophicum (strain De)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
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                    RYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWGETWEKAKTMCEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETWEKAKTMCECYD-----YLFDIAVSMKK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | : | |||
EGLRDALLLAEFIEESARTQFIAETLKSMKK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: MTH1406
A;Start codon: GTG
C;Superfamily: L-ribulose-phosphate 4-epimerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-fuculose-phosphate aldolase homolog
                                                                                                                                                                                                                      214 YDYLFD 219
                                                                                                                                                                                                                                                                               :::||:
190 FEFLFE 195
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Best Local Similarity
Matches 52; Conserv
                    154
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                                    C. Species: Aquitex acolicus
C. Species: Aquitex acolicus
C. Species: Aquitex acolicus
C. Species: Aquitex acolicus
C. Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C. Accession: H70469
R. Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov V. Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov V. Deckert 392, 353-358, 1998
A. Title: The complete genome of the hyperthermophilic bacterium Aquifex acolicus.
A. Reference number: A70300; MUD: 98196666; PMID: 9537320
A. Residual Day A. Mulanary; nucleic acid sequence not shown; translation not shown
A. Molecule type: DNA
A. Residuals: 1-208 c.AQFP.
A. Residuals: 1-208 c.AQFP.
A. Cross-references: UNIPROY: O67788; GB: AE000766; GB: AE000657; NID: 92984216; PIDN: AAC0775
A. Experimental source: strain VFS
C. Genetics:
A. Gen
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C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Accession: D83436
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradanan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Hickey, M.J.; Brady, J.C.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A,Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathoth; Reference number: A82950; MUID:20437337; PMID:10984043
A,Accession: D83436
A,Accession: preliminary
A,Molecule type: DNA
A,Residues: 1-205 <STO>
A,Residues: 1-205 <STO
A,Residues: 1-205 <STO
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fuculose-phosphate aldolase homolog - Aquifex aeolicus
Species: Aquifex aeolicus
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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12.6%; Score 166; DB 2; Length 205;
Best Local Similarity 26.3%; Pred. No. 1.6e-07;
Matches 49; Conservative 29; Mismatches 96; Indels
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Local Similarity 25.1%; Pred. No. 6.6e-10;
Ne 53; Conservative 37; Mismatches 94
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Best Local Si
Matches 53;
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Gene: PA1683
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A; Experimental source: strain K-12, substrain MG1655
R; Blattner, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
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R, anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A,Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A,Reference number: A82515, MID:20365717, PMID:10910347
A,Note: for a complete list of authors see reference number A59328 below
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A; Residues: 1-218 cXIN-
A; Residues: 1-218 cXIN-
A; Cross-references: UNIPROT: QPBDD5; GB: AE004033; GB: AE003849; NID: g9107342; PIDN: AAP8500
A; Cross-references: UNIPROT: QPBDD5; GB: AE004033; GB: AE003849; NID: g9107342; PIDN: AAP8500
B; Experimental Bource: grain 9a5c
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
Submitted to GenBank, June 2000
A; Authors: Perreira, W.L.; Kemper, B.L.; Kitajima, J.P.; Kranger, J.E.; Kuranae, E.E.; Laigri
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, E.M.F.; Matukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Numes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Salve, M.A.; da Silva, A.M.; Silva Jr., W.A.; da Silvair, M.A.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.
                                                                                                       EMBL:U00039; NID:g466582; PIDN:AAB18560.1; PID:g4667
                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: GB:AE000435; GB:U00096; NID:g2367244; PIDN:AAC76607.1; PID:g1790008; A,Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein XF2209 [imported] - Xylella fastidiosa (strain 9a5c)
C,Species: Xylella fastidiosa
C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ASGKVVEGSKKPSSDTPTHLALYRRYAEIGGIVHTHSRHATIWSQAGLDLPA--WGTTHA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 EMIKGIKKCTS-----GGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LAANLALPAHHL--VTFTWGNVSAV--DETRQWNVIKPSGVEYDVMTADDMVVVEI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 ISGPSPSKKLKKSOCTPLFMNAYTWRG-AGAVIHTHSKAAVM---ATLLFPGREFKITHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 DYFYGAIPCTROMTABEINGEYEYO ---TGEVIIETFEERG-----RSPAQIP---AVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 LIPELCKOFYHLGWVTGTGGGISLKHGDE----IYIAPSGVQKERIQPEDMFVCDINEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 VRRHGVYVWG----ETWEKAKTMCEC-YDYLFDIAVSMKKVGLDPSQLPVGENGIV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: isomerase; zinc
F;76,95,97,171/Binding site: zinc (Asp, His, His, His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 231;
                                                                                                                                                                                                            91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.0%; Score 145; DB 2; 28.8%; Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: L-ribulose-phosphate 4-epimerase
                                                                             A, Residues: 1-231 <PLU>
A, Cross-references: UNIPROT: P37680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 28.89
                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-231 < BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary A;Molecule type: DNA
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A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A,Feference number: A72200; MUID:99287316; PMID:10360571
A,Accession: A72396
A,Status: preliminary
A,Nolecule type: DNA
A,Residues: 1-254 <ARN>
A,Experimental Eyes : UNIPROT:Q9WYB9; GB:AE001710; GB:AE000512; NID:g4980775; PIDN:AAD3537
A,Cross-references: UNIPROT:Q9WYB9; GB:AE001710; GB:AE000512; NID:g4980775; PIDN:AAD3537
A,Gene: TM0283
C,Genetics:
A,Gene: TM0283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A72396
L-fuculose-phosphate aldolase homolog - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: A72396
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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S47804

L-ribulose-phosphate 4-epimerase homolog (EC 5.1.3.-) yiaS - Escherichia coli (strain P N/Alternate names: hypothetical protein 0231

C;Species: Escherichia coli
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004

C;Accession: S47804; A65158

Splunkett, G.
Submitted to the EMBL Data Library, March 1994

A;Reference number: S47666
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                                                                                                                                                                                                                                                                                                                                        SGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKSQCTPLFMNAYTMRGAGAVIHTHSKA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AVMATLLFPGREFKITHQEMIKGIKKCTSGGYYRYDDML--VVPIIENTP-EEKGLKDRM 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CDAGEGDCCSRRCGAQ---DKEHPRYLIPELCKQFYHLGWVTGTGGGISLKHGDEIYIAP
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                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---DEDVIILKNHGVVCLGK 154
                                                                                                                                                                                                                                                                                                                                                                                                                   SGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWGE 202
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                                                                                   Length 181;
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11.4%; Score 151; DB 1;
Best Local Similarity 27.1%; Pred. No. 4.7e-06;
Matches 57; Conservative 36; Mismatches 95;
                                                                                Score 152; DB 1;
Pred. No. 2.5e-06;
                                                               11.5%; bcc. No. 2.2.24.7%; Pred. No. 2.2.36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 AHAMNEYPDSCAVLVRRHGVYVWGETWEKA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKVIGK---SGAVLLRKHGVMIVGTSVDDA 209
A,Map position: FOR1381152-1381697
C;Superfamily: L-ribulose-phosphate 4-epimerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GYVDYYEAGSLKLAEETAKR----
                                                                                                                                       Conservative
                                                                                                          Similarity
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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad Sci. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Residues: 1-244 - ....
A,Cross-references: UNIPROT: Q8YDI7; GB: AE008918; PIDN: AAL53430.1; PID:g17984327; GSPDB:C
A,Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-fuculose phosphate aldolase (EC 4.1.2.17) [imported] - Brucella melitensis (strain 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 SDTATHLALYRRYPQ--IGGIVHTHSRHATIWSQAGLDLPA--WGTTHADYFYGAIPCTR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 KSQCTPLFM-NAYTMRGAGAVIHTHSKAAVM---ATLLFPGREFKITHQEMIKGIKKCTS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 LMTVEEINGEYEYQ---TGEVIIKTFEERGLDPA-----QIP---AVLVHSHGPFAWGK 178
                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-231 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07949.1; PID:g16504938; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWG- 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLVIFTWGNVSAV--DETRKLMVIKPSGVEYBVMTADDMVVVBIASGKVVEG---NKKPS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 ROSIVDAMRSFEEKGFNHGSSGNISVREGGHIWVTPTGA-TSTMDPQDMSLVSLEGEHLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GWVTGTGGGISLKHGDE----IYIAPSGVQKERIQPEDMFVCDI-NEKDISGPSPSKKLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
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Pred. No. 3.4e-05;
6; Mismatches 84;
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; Pred. No. 4e-0
31; Mismatches
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C;Keywords: aldehyde-lyase; carbon-carbon lyase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%;
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23.8%;
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ses 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: STY4119
C;Superfamily: L-ribu:
C;Keywords: isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: AC3533
A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein SP2033 [imported] - Streptococcus pneumoniae (strain TIGR4)
C; Species: Streptococcus pneumoniae
C; Species: Streptococcus pneumoniae
C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C; Accession: A95238
C; Accession: A95238
R; Tetteflin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Science 293, 496-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A; Recession: A95238
A; Reference number: A95000; MUID:21357209; PMID:11463916
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-227 «KUR»
A; Residues: 1-2
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A10977
probable sugar isomerase (EC 5.1.-.-) [imported] - Salmonella enterica subsp. enterica
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                                                                                                                                                                                                                                                                                                                                               92 LKKSQCTPLFMNAY-TWRGAGAVIHTHSKAAVMATLLFPGR-EFKITHQEMIKGIKKCTS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGYYRYDDMLVVPIIENTPEEKGL-----KDRMAHAMNEYPDSCAVLVRRHGVYVW 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 -GHSTHETTLDVPVFCNTQNMNILAAQVDTLLDKQRM-------WGYLINGHGMYTW 187
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                                                                                                                                                                                                                                          34 OFYHLGWVTGTGGGISLKHGD-EIYIAPSGVQKERIQPEDMFVCDINEKDISGP-SPSKK 91
                                                                                                                                                                                                                                                                                                                                                                                ----GYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWGETWE
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                                                                                                                                      Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 10.7%; Score 142; DB 2; Length 22 Local Similarity 30.8%; Pred. No. 2.7e-05; Nes 56; Conservative 22; Mismatches 72; Indels
                                                                                                                                                                                        Indels
                                                                                                                                                                                     92;
                                                                                                                                   10.9%; Score 144; DB 2; 23.7%; Pred. No. 1.7e-05;
                                                                                                                                                                                        32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | :: | :: |: GNTLADARRHLEALEFLIHCELNLIKL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GETWEKAKTMCECYDYLFDIAVSMKKV 227
                                                                                                                                                                                        Conservative
Reference number: A59328
Contents: annotation
Genetics:
                                                                                                                                                            Similarity
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                                                                                                                                                                                     49;
                                                                              A; Gene: XF2209
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Matches
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L-ribules
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L-ribules
L-ribules
Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B98102
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E, R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; W.; P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Tetus: preliminary
A;Residues: 1-234 akuns.
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Coss-references: UNIPROT:Q8DN99; GB:AE007317; PIDN:AAL00647.1; PID:g15459534; GSPDB:C
C;Genetics:
A;Gene: arab
C;Superfamily: L-ribulose-phosphate 4-epimerase
C;Keywords: isomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWGETWE 205
129 PGREFKITHQEMIKGIKKCTSGGYYRY--DDMLVVPIIENTPEEKGLKDRMAHANNEYPD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 GWYTGTGGGISLKHGD--EIYIAPSGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKSQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 GLVKFTWGNVSEVNRELGVIVIKPSGVDYDELTPENMVVTDLDGKILEG----DLRPSS 77
                                                                                                                                         ------RÁMGHHR- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
10.4%; Score 137; DB 2; Length 234;
Best Local Similarity 30.2%; Pred. No. 7.8e-05;
Matches 55; Conservative 22; Mismatches 73; Indels 32; Gaps
                                                                                                                                      148 GGSEV-----PCAS---YRVFGSDALAYEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: February 1, 2005, 14:30:13 Job time: 42 secs
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